



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lin, Yao-Zhong
Bawiger, Jack J.

(ii) TITLE OF INVENTION: A NOVEL METHOD FOR IMPORTING
BIOLOGICALLY ACTIVE MOLECULES INTO CELLS

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/516,310
- (B) FILING DATE: 2000-03-01
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Perryman, David G.
- (B) REGISTRATION NUMBER: 35,438
- (C) REFERENCE/DOCKET NUMBER: 22000.0021U2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 404/688-0770
- (B) TELEFAX: 404/688-9880

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= a
/note= "Signal peptide amino acid sequence of
K-EGF"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 17..19
- (D) OTHER INFORMATION: /label= b
/note= "Spacer region"

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 20..26
- (D) OTHER INFORMATION: /label= c
/note= "Epitope tag"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 1 5 10 15

Ala Ala Ala Asp Gln Asn Gln Leu Met Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME KEY: Peptide
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /label= a
 /note= "Nuclear localization sequence of aFGF"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Tyr Lys Lys Pro Lys Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= a
 /note= "Signal peptide amino acid sequence of K-PHF"

(ix) FEATURE:

- (A) NAME KEY: Peptide
- (B) LOCATION: 17..18
- (D) OTHER INFORMATION: /label= b
 /note= "Spacer region"

(ix) FEATURE:

- (A) NAME KEY: Peptide
- (B) LOCATION: 20..26
- (D) OTHER INFORMATION: /label= c
 /note= "Nuclear localization sequence of aFGF"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 1 5 10 15

Ala Ala Ala Asn Tyr Lys Lys Pro Lys Leu
 1 5 10 25

(1) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= a
 (note= "Signal peptide amino acid sequence of K-EGF")

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 17..19
- (D) OTHER INFORMATION: /label= b
 (note= "Spacer region")

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 20..26
- (D) OTHER INFORMATION: /label= c
 (note= "Nuclear localization sequence of aEGF")

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 26..28
- (D) OTHER INFORMATION: /label= d
 (note= "Epitope tag")

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
 1 5 10 15
 Ala Ala Ala Asn Tyr Lys Lys Pro Lys Leu Met Pro
 20 25

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..16
- (D) OTHER INFORMATION: /label= a
 (note= "Signal peptide of K-EGF")

SEQ. ID NO:5: SEQUENCE DESCRIPTION: SEQ. ID NO:5:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

Glu Ile Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr
20 25 30

Pro Gly Met Phe Ile Ala Leu Ser Lys
35 40

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Ile Leu Leu Pro Asn Asn Tyr Asn Ala Tyr Glu Ser Tyr Lys Tyr
1 5 10 15

Pro Gly Met Phe Ile Ala Leu Ser Lys
20 25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu
20 25

(1) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Ala Val Ala Leu Leu Pro Ala Val Leu Leu Ala Leu Leu Ala Pro
1 5 10 15

Val Asn Arg Lys Arg Asn Lys Leu Met Pro
20 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Asn Arg Lys Arg Asn Lys Leu Met Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Glu Glu Lys Arg Lys Arg Thr Tyr Glu
1 5 10